SEQUENCE LISTING

	"\
5	(1) GENERAL INFORMATION:
5	(i) APPLICANTS: Vassilios Papadopoulos
	Martine Culty
	(ii) TITLE OF INVENTION: Peripheral-type Benzodiazepine Receptor:
10	A Tool for Detection, Diagnosis, Prognosis, and Treatment of Cancer
	(iii) NUMBER OF SEQUENCES: 3
	() CORDERON TENER A PROPERTY
4.5	(iv) CORRESPONDENCE ADDRESS:
15	(A) ADDRESSEE: Pratt & Associates, Inc.
	(B) STREET: 10821 Hillbrooke Lane
	(C) CITY: Potomad (D) STATE: MARYLAND
	(E) COUNTRY: USA
20	(E) COUNTRY : USA (F) ZIP: 20854
20	(1) ZH . 20054
	(v) COMPUTER READABLE FORM:
	(A) MEDIUM TYPE: Floppy disk
	(B) COMPUTER: Apple Macintosh
25	(C) OPERATING SYSTEM: Macintosh 7.5
	(D) SOFTWARE: Microsoft Word 6.0
	(vi) CURRENT APPLICATION DATA:
	(A) APPLICATION NUMBER:
30	(B) FILING DATE:
	(C) CLASSIFICATION:
	(vii) PRIOR APPLICATION DATA:
	(A) APPLICATION NUMBER:
35	(B) FILING DATE: \
33	(B) I IEM (S BITTE:
	(viii) ATTORNEY/AGENT INFORMATION:
	(A) NAME: Sana A. Pratt
	(B) REGISTRATION NUMBER: 39,441
40	(C) REFERENCE/DOCKET NUMBER: 009/064/SAP
	() THE ECONO (DICAMION TO THE ONLY
	(ix) TELECOMMUNICATION INFORMATION
	(A) TELEPHONE: (301)294-9171 (B) TELEFA V. (201)204-7257
<i>1</i> E	(B) TELEFAX: (301)294-7357
45	(2) INFORMATION FOR SEQ ID NO:1:
	(2) IN ORDINATION TORBEQ ID NO.1.
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 652 base pairs \
50	(B) TYPE: Nucleic acid \
	(C) STRANDEDNESS: Single \

(D) TOPOLOGY: Linear

(ii) SEQUENCE DESCRIPTION: SEQ ID NO:1:

		1					
5	CCACGGCGAA	GGTCTCCGCT	GGTACGCCGG	CCTGCAGAAG	40		
	CCCTCGTGGC	ACCCGCCCCA	CTGGGTGCTG	GGCCCTGTCT	80		
	GGGCACGCT	CTACTCAGCC	ATGGGGTACG	GCTCCTACCT	120		
	GGTCTGGAAA	GAGCTGGGAG	GCTTCACAGA	GAAGGCTGTG	160		
	GTTCCCCTGG	GCCTCTACAC	TGGGCAGCTG	GCCCTGAACT	200		
10	GGGCATGGCC	CCCCATCTTC	TTTGGTGCCC	GACAAATGGG	240		
	CTGGGCCTTG	GTGGATCTCC	TGCTGGTCAG	TGGGGCGCG	280		
	GCAGCCACTA	CCGTGGCCTG	GTACCAGGTG	AGCCCGCTGG	320		
	CCGCCCGCCT	GCTCTACCCC	TACCTGGCCT	GGCTGGCCTT	360		
	CACGACCACA	CTCAACTACT	GCGTATGGCG	GGACAACCAT	400		
15	GGCTGGCGTG	GGGGACGGCG	GCTGCCAGAG	TGAGTGCCCG	440		
	GCCCACCAGG	GACTGCAGCT	GGACCAGCAG	GTGCCATCAC	480		
	GCTTGTGATG	TGGTGGCCGT	CACGCTTTCA	TGACCACTGG	520		
	GCCTGCTAGT	CTGTCAGGGC	CTTGGCCCAG	GGGTCAGCAG	560		
	AGCTTCAGAG	GTGGCCCCAC	CTGAGCCCCC	ACCCGGGAGC	600		
20	AGTGTCCTGT	GCTTTCTGCA	TGCTTAGAGC	ATGTTCTTGG	640		
	AACATGGAAT	TT			652		
	(3) INFORMA						
25		UENCE CHAR. (A) LENGTH: 6 (B) TYPE: Nuclo (C) STRANDEI (D) TOPOLOGY	552 base pairs eic acid ONESS: Single				
30	(ii) SEQUENCE DESCRIPTION: SEQ TO NO:2:						

CCACGGCGAG GGTCTCCGCT GGTACGCCGG CCTGCAGAAG

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	CCCTCGTGGC	ACCCGCCCCA	CTGGGTGCTG	GGCCCTGTCT	80
	GGGGCACGCT	CTACTCAGCC	ATGGGGTACG	GCTCCTACCT	120
	GGTCTGGAAA	GAGCTGGGAG	GCTTCACAGA	GAAGGCTGTG	160
	GTTCCCCTGG	GCCTCTACAC	TGGGCAGCTG	GCCCTGAACT	200
5	GGGCATGGCC	CCCCATCTTC	TTTGGTGCCC	GACAAATGGG	240
	CTGGGCCTTG	GTGGATCTCC	TGCTGGTCAG	TGGGGCGGCG	280
	GCAGCCACTA	CCGTGGCCTG	GTACCAGGTG	AGCCCGCTGG	320
	CCGCCCGCCT	GCTCTACCCC	TACCTGGCCT	GGCTGGCCTT	360
	CACGACCACA	CTCAACTACT	GCGTATGGCG	GGACAACCAT	400
10	GGCTGGCGTG	GGGGACGGCG	GCTGCCAGAG	TGAGTGCCCG	440
	GCCCACCAGG	GACTGCAGCT	GCACCAGCAG	GTGCCATCAC	480
	GCTTGTGATG	TGGTGGCCGT	CACGCTTTCA	TGACCACTGG	520
	GCCTGCTAGT	CTGTCAGGGC	CTTGGCCCAG	GGGTCAGCAG	560
	AGCTTCAGAG	GTGGCCCCAC	CTGAGCCCCC	ACCCGGGAGC	600
15	AGTGTCCTGT	GCTTTCTGCA	TGCTTAGAGC	ATGTTCTTGG	640
	AACATGGAAT	TT \			652

(4) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) TOPOLOGY: Linear

25 (ii) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa 1 5 \ 10

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa 30 15 20

Xaa Xaa Xaa Xaa Xaa His Gly Glu Gly
25 30

35 Leu Arg Trp Tyr Ala Gly Leu Gln Lys Pro

		1	١		35					40
	Ser	Trp	His	Pro	Pro 45	His	Trp	Val	Leu	
5	Pro	Val	Trp	Gly	Thr 55	Leu	Tyr	Ser	Ala	Met 60
10	Gly	Tyr	Gly/	Ser	Tyr 65	Leu	Val	Trp	Lys	Glu 70
	Leu	Gly	Gly	Phe	Thr 75	Glu	Lys	Ala	Val	Val 80
15	Pro	Leu	Gly	Leu	Tyr 85	Thr	Gly	Gln	Leu	Ala 90
	Leu	Asn	Trp	Ala	Trp 95	Pro	Pro	Ile	Phe	Phe 100
20	Gly	Ala	Arg	Gln	Met 105	Gly	Trp	Ala	Leu	Val 110
25	Asp	Leu	Leu	Leu	Val 115	Ser	Gly	Ala	Ala	Ala 120
	Ala	Thr	Thr	Val	Ala 125	Trp	Tyr	Gln	Val	Ser 130
30	Pro	Leu	Ala	Ala	Arg\ 135		Leu	Tyr	Pro	Tyr 140
2.5	Leu	Ala	Trp	Leu	Ala 145	Phe	Thr	Thr	Thr	Leu 150
35	Asn	Tyr	Cys	Val	Trp 155	Arg	Asp	Asn	His	Gly 160
40	Trp	Arg	Gly	Gly	Arg 165	Arg	Leu	Pro	Glu	